What is claimed is:

1. A substantially purified nucleic acid molecule expressed in response to polycyclic aromatic hydrocarbon exposure comprising:

(a) a nucleic acid molecule encoding a protein selected from SEQ ID NOs:7, 8 and 14;

(b) a nucleic acid molecule selected from the group consisting of SEQ ID NOs:1-5 and 9-13; or

(c) a nucleic acid molecule which is the complement of the nucleic acid molecule of (a) or (b) wherein each and every nucleotide of the complement is complementary to each and every nucleotide of the nucleic acid molecule of (a) or (b).

2. A substantially purified nucleic acid molecule expressed in response to polycyclic aromatic hydrocarbon exposure comprising:

(a) a nucleic acid molecule encoding a protein of SEQ ID NO:6; or

(b) a nucleic acid molecule which is the complement of the nucleic acid molecule of (a) wherein each and every nucleotide of the complement is complementary to each and every nucleotide of the nucleic acid molecule of (a).

3. A method of using a nucleic acid molecule to screen a library of molecules or compounds to identify at least one ligand which specifically binds the nucleic acid molecule, the method comprising:

(a) combining the nucleic acid molecule of claim 1 with a library of molecules or compounds under conditions to allow specific binding; and

(b) detecting specific binding, thereby identifying a ligand which specifically binds the nucleic acid molecule.

4. A method of using a nucleic acid molecule to screen a library of molecules or compounds to identify at least one ligand which specifically binds the nucleic acid molecule, the method comprising:

(a) combining the nucleic acid molecule of claim 2 with a library of molecules or compounds under conditions to allow specific binding; and

(b) detecting specific binding, thereby identifying a ligand which specifically binds the nucleic acid molecule.

5. The method of claim 3 wherein the library is selected from DNA molecules, RNA molecules, peptide nucleic acids, mimetics, and proteins.

6. The method of claim 4 wherein the library is selected from DNA molecules, RNA molecules, peptide nucleic acids, mimetics, and proteins.

7. A ligand identified by the method of claim 3 which modulates the activity of the nucleic acid

molecule.

8. A ligand identified by the method of claim 5 which modulates the activity of the nucleic acid molecule.

9. A method of using a nucleic acid molecule to purify a ligand which specifically binds the nucleic acid molecule, the method comprising:

(a) combining the nucleic acid molecule of claim 1 with a sample under conditions to allow specific binding;

(b) detecting specific binding between the nucleic acid molecule and a ligand;

(c) recovering the bound nucleic acid molecule; and

(d) separating the nucleic acid molecule from the ligand, thereby obtaining purified ligand.

10. A method of using a nucleic acid molecule to purify a ligand which specifically binds the nucleic acid molecule, the method comprising:

(a) combining the nucleic acid molecule of claim 2 with a sample under conditions to allow specific binding;

(b) detecting specific binding between the nucleic acid molecule and a ligand;

(c) recovering the bound nucleic acid molecule; and

(d) separating the nucleic acid molecule from the ligand, thereby obtaining purified ligand.

11. A method for diagnosing a disorder or condition associated with the altered expression of a gene expressed in response to polycyclic aromatic hydrocarbon exposure in a plurality of biological samples, the method comprising the steps of:

(a) hybridizing a nucleic acid molecule of claim 1 to a sample under conditions effective to form one or more hybridization complexes;

(b) detecting the hybridization complexes; and

(c) comparing the levels of the hybridization complexes with the level of hybridization complexes in a control sample, wherein the altered level of hybridization complexes compared with the level of hybridization complexes of a control sample indicates the presence of the disorder or condition.

12. A method for diagnosing a disorder or condition associated with the altered expression of a gene expressed in response to polycyclic aromatic hydrocarbon exposure in a plurality of biological samples, the method comprising the steps of:

(a) hybridizing a nucleic acid molecule of claim 2 to a sample under conditions effective to form one or more hybridization complexes;

(b) detecting the hybridization complexes; and

(c) comparing the levels of the hybridization complexes with the level of hybridization

complexes in a control sample, wherein the altered level of hybridization complexes compared with the level of hybridization complexes of a control sample indicates the presence of the disorder or condition.

13. A method for detecting or diagnosing effect of a compound on expression level of at least one nucleic acid molecule in a subject, the method comprising:

(a) treating the subject with the compound;

(b) obtaining a sample containing nucleic acid molecules from the subject;

(c) contacting the sample with at least one nucleic acid molecule of claim 1 under conditions for the formation of hybridization complexes; and

(d) detecting at least one hybridization complex, wherein the presence, absence, or change in amount of hybridization complex when compared with hybridization complex formed with a sample from an untreated subject indicates the effect of the compound.

14. A method for detecting or diagnosing effect of a compound on expression level of at least one nucleic acid molecule in a subject, the method comprising:

(a) treating the subject with the compound;

(b) obtaining a sample containing nucleic acid molecules from the subject;

(c) contacting the sample with at least one nucleic acid molecule of claim 2 under conditions for the formation of hybridization complexes; and

(d) detecting at least one hybridization complex, wherein the presence, absence, or change in amount of hybridization complex when compared with hybridization complex formed with a sample from an untreated subject indicates the effect of the compound.

15. A substantially purified protein expressed in response to polycyclic aromatic hydrocarbon exposure, comprising

(a) a protein selected from SEQ ID NOs:6-8 or a portion thereof; and

(b) an oligopeptide comprising at least 6 sequential amino acids of the protein of (a); and

(c) an immunogenic fragment of the protein of (a).

16. A protein of claim 15, comprising the amino acid sequence of SEQ ID NO:6.

17. A protein of claim 15, comprising the amino acid sequence of SEQ ID NO:7.

18. A protein of claim 15, comprising the amino acid sequence of SEQ ID NO:8.

19. A composition comprising a protein of claim 15 and a pharmaceutical carrier.

20. A method for using a protein to screen a library of molecules or compounds to identify at least one ligand which specifically binds the protein, the method comprising:

(a) combining the protein of claim 15 with the library of molecules or compounds under conditions to allow specific binding; and

(b) detecting specific binding between the protein and ligand, thereby identifying a ligand which specifically binds the protein.

21. The method of claim 20 wherein the library is selected from DNA molecules, RNA molecules, peptide nucleic acids, mimetics, proteins, agonists, antagonists, and antibodies.

22. A ligand identified by the method of claim 20 which modulates the activity of the protein.

23. A method of using the protein to purify a ligand from a sample, the method comprising:

(a) combining the protein of claim 15 with a sample under conditions to allow specific binding;

(b) detecting specific binding between the protein and a ligand;

(c) recovering the bound protein; and

(d) separating the protein from the ligand, thereby obtaining purified ligand.

24. An antibody which specifically binds to the protein of claim 15.

25. A diagnostic test for a condition or disease associated with the expression of a protein in a biological sample comprising the steps of:

(a) combining the biological sample with an antibody of claim 24, under conditions suitable for the antibody to bind the protein and form an antibody:protein complex; and

(b) detecting the complex, wherein the presence of the complex correlates with the presence of the protein in the biological sample.

26. The antibody of claim 24, wherein the antibody is:

(a) a chimeric antibody;

(b) a single chain antibody;

(c) a Fab fragment;

(d) a $F(ab')_2$ fragment, or

(e) a humanized antibody.

27. A composition comprising an antibody of claim 24 and an acceptable excipient.

28. A method of diagnosing a condition or disease associated with the expression of a protein in a subject, comprising administering to said subject an effective amount of the composition of claim 26.

29. A composition of claim 26, wherein the antibody is labeled.

30. A method of diagnosing a condition or disease associated with the expression of a protein in a subject, comprising administering to said subject an effective amount of the composition of claim 29.

31. A method of preparing a polyclonal antibody comprising:

(a) immunizing an animal with a protein of claim 15 under conditions to elicit an antibody

response;

(b) isolating antibodies from said animal; and

(c) screening the isolated antibodies with the protein thereby identifying a polyclonal antibody which binds specifically to a protein of SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:8.

32. An antibody produced by a method of claim 31.

33. A composition comprising the antibody of claim 32 and a suitable carrier.

34. A method of making a monoclonal antibody comprising:

(a) immunizing an animal with a protein of claim 15 under conditions to elicit an antibody response;

(b) isolating antibody producing cells from the animal;

(c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-producing hybridoma cells;

(d) culturing the hybridoma cells; and

(e) isolating from the culture monoclonal antibody which binds specifically to a protein of SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:8.

35. A monoclonal antibody produced by a method of claim 34.

36. The antibody of claim 24, wherein the antibody is produced by screening a Fab expression library.

37. The antibody of claim 24, wherein the antibody is produced by screening a recombinant immunoglobulin library.

38. A method for detecting a protein in a sample comprising the steps of:

(a) incubating the antibody of claim 24 with a sample under conditions to allow specific binding of the antibody and the protein; and

(b) detecting specific binding, wherein specific binding indicates the presence of a protein of SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:8 in the sample.

39. A method of purifying a protein from a sample, the method comprising:

(a) incubating the antibody of claim 24 with a sample under conditions to allow specific binding of the antibody and the protein; and

(b) separating the antibody from the sample and obtaining purified protein of SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:8.

TABLE 1

Rat SEQ ID NO	Rat Incyte ID No.	Human SEQ ID NO.	Human Incyte ID No.	Unique Fragment	Identity	Human Tissue Expression Profile
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11	700367683	3	253053	690-740	61.3%	31% reproductive tissue and 25% nervous tissue
12	701316810	4	2009569	327-368	95.4%	67% reproductive tissue
13	700139271	5	1642580	196-231	49.3%	44% liver tissue and 22% hematopoietic/immune tissue

PB-0011 US

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				335				340						345	

Ala Thr Arg Asn Glu Glu Leu Asn Leu Leu Arg Asn Val Asp Ala
350 355 360
Asn Asn Thr Glu Asn Ser Thr Thr Val Lys Asn Ser Ser Leu Leu
365 370 375
Ser Gly Phe Arg Gly Gly Ser Ser Tyr Asn His Glu Thr Glu Thr
380 385 390
Ile Phe Ala Leu Pro Arg Met Gln Leu Asp Phe Lys Ser Ile His
395 400 405
Val Gln Glu Pro Gln Glu Pro Ser Leu Gln Asp Ala Ser Leu Lys
410 415 420
Pro Lys Val Glu Cys Ser Val Val Thr Glu Phe Thr Asp His Ile
425 430 435
Cys Val Thr Met Asp Ala Glu Leu Ile Met Phe Leu His Asp Leu
440 445 450
Val Ser Ala Tyr Leu Lys Glu Lys Glu Lys Ala Ile Phe Pro Pro
455 460 465
Arg Ile Leu Ser Thr Arg Pro Gly Gln Lys Ser Pro Ile Ile Ile
470 475 480
His Asp Asp Asn Ser Ser Asp Lys Asp Arg Glu Asp Ser Ile Thr
485 490 495
Tyr Thr Thr Val Asp Trp Arg Asp Phe Met Cys Asn Thr Trp His
500 505 510
Leu Glu Pro Thr Leu Arg Leu Ile Ser Trp Thr Gly Arg Lys Ile
515 520 525
Asp Pro Val Gly Val Asp Tyr Ile Leu Gln Lys Leu Gly Phe His
530 535 540
His Ala Arg Thr Thr Ile Pro Lys Trp Leu Gln Arg Gly Val Met
545 550 555
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Glu His

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35 40 45
Ser Cys Gln Leu Thr Val Leu Glu Gly Lys Ser Gly Leu Tyr Phe
50 55 60
Ser Ser Leu Asp Ser Ser Ile Asp Ile Leu Gln Lys Arg Ala Gln
65 70 75
Glu Leu Ile Glu Asn Ile Asn Lys Ser Arg Gln Lys Asp His Ala
80 85 90
Leu Met Thr Asn Phe Arg Asn Ser Leu Lys Thr Lys Val Ser Asp
95 100 105
Leu Thr Glu Lys Leu Glu Glu Arg Ile Tyr Gln Ile Tyr Asn Asp
110 115 120
His Asn Lys Ile Ile Gln Glu Lys Leu Gln Glu Phe Thr Gln Lys
125 130 135
Met Ala Lys Ile Ser His Leu Glu Thr Glu Leu Lys Gln Val Cys

His Ser Val Glu Thr Val Tyr Lys Asp Leu Cys Leu Gln Pro Glu
Gln Ser Leu Arg Leu Arg Trp Gly Pro Asp His Ser Arg Gly Lys
Ser Pro Pro Arg Pro Gly Asn Ser Gln Pro Pro Asp Val Phe Val
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Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala
Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Arg Asp
Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg
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gagacagaga agacggcatc acttacacca ctgtggactg gcgagacttt atgtgtaaca 180
catggcatct ggagcctact cttagattaa tttcttggac tggaagaaag attgatccag 240
taggtgttga ttacattctt caaaaattgg gctttcacca tgccaggact actattccca 300
aatggcttca gagaggagtg atggacccac tggataaggt gctatccgtt ctcatcaaaa 360
aactcgggac tgccctgcag gatgagaagg agaagaaagg aaaagacaaa gaagaacact 420
agaatagtaa ctccatctgt gaagtacctg actctgtccg ttaagttctg gcactgcaat 480
tttttcagca taactttaaa tggtacttca aaataattct aattttgtgg ccattattga 540
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ctccctctac ttcctcctct ggattcctga ggaccagcca tcttgggtca gtgccctggt 180
caagtgccag cccattctct gcctggtttt gttcctgtgg gctgtggctc ctggtgggag 240
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gtgtctaaat ctccagtctg tctgttgtac tggtaattta actctgtaat ggaatagttt 180
gctgccaact atttatatta agtcattttt aaatatttgt aatattgttg actgactaat 240
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gaaatggagc tcaaacaagt ttgccaaact gtggaaacta tgtacaagga cctatgtgtc 180
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acagacgaga cagactacgg ctctgcagcc ttggcatggg gcagaaagca agactgatga 180
cagtgcgctg ctgatgctga agcgaaggaa gcgagacacc aacttcccca tatgcctctt 240
ctgctgtaaa tgctgtaaga attcctcctg tggtctctgt tgcataacat agagagccaa 300
gagccttgtc ctgacctctc aacacactgc ctcccctccg ccccattatt tattcctgtc 360
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Leu Leu Ala Ser Leu Ser Ser Gly Ala Tyr Leu Arg Gln Gln Thr
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Arg Gln Thr Thr Ala Leu Gln Pro Trp His Gly Ala Glu Ser Lys
35 40 45
Thr Asp Asp Ser Ala Leu Leu Met Leu Lys Arg Arg Lys Arg Asp
50 55 60
Thr Asn Phe Pro Ile Cys Leu Phe Cys Cys Lys Cys Cys Lys Asn
65 70 75
Ser Ser Cys Gly Leu Cys Cys Ile Thr
80